

**WHAT IS CLAIMED IS:**

1. An isolated nucleic acid molecule encoding a BEL transcription factor from *Solanum tuberosum*.

5 2. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

10 3. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid sequence encodes a protein that is at least 85% similar to a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default  
15 parameters analysis.

4. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent conditions characterized by a  
20 hybridization buffer comprising 5X SSC at a temperature of 55°C.

25 5. The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

30 6. The isolated nucleic acid molecule according to claim 2, wherein the nucleic acid molecule encodes a protein or polypeptide having a molecular mass of about 56 kDa to about 76 kDa.

7. A DNA construct comprising:  
the nucleic acid molecule according to claim 1, and  
an operably linked promoter and 3' regulatory region.

5 8. An expression vector comprising the DNA construct of  
claim 7.

9. The expression vector according to claim 8, wherein the  
nucleic acid molecule is in proper sense orientation and correct reading frame.

10 10. A host cell transduced with the nucleic acid molecule  
according to claim 1.

11. The host cell according to claim 10, wherein the cell is  
selected from the group consisting of a bacterial cell, a virus, a yeast cell, an insect  
cell, a plant cell, and a mammalian cell.

12. A transgenic plant transformed with the nucleic acid  
molecule according to claim 1.

20 13. The transgenic plant according to claim 12, wherein the  
nucleic acid molecule has a nucleotide sequence selected from the group  
consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ  
ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

25 14. The transgenic plant according to claim 12, wherein the  
nucleic acid sequence encodes a protein that is at least 85% similar to a  
homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box in  
either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID  
NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default  
parameters analysis.

15. The transgenic plant according to claim 12, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent conditions characterized by a hybridization buffer  
5 comprising 5X SSC at a temperature of 55°C.

16. The transgenic plant according to claim 12, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4,  
10 SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

17. The transgenic plant according to claim 12, wherein the nucleic acid molecule encodes a protein or polypeptide having a molecular mass  
15 of about 56 kDa to about 76 kDa.

18. The transgenic plant according to claim 12, wherein the plant is selected from the group consisting of Gramineae, Liliaceae, Iridaceae, Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae, Rosaceae,  
20 Leguminosae, Malvaceae, Umbelliferae, Labiate, Solanaceae, Cucurbitaceae, Compositae, and Rubiaceae.

19. A transgenic plant seed transformed with the nucleic acid molecule according to claim 1.  
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20. The transgenic plant seed according to claim 19, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

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21. The transgenic plant seed according to claim 19, wherein the nucleic acid sequence encodes a protein that is at least 85% similar to a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box in

either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis.

5           22.     The transgenic plant seed according to claim 19, wherein  
the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1,  
SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or  
SEQ ID NO:13 under stringent conditions characterized by a hybridization buffer  
comprising 5X SSC at a temperature of 55°C.

10           23.     The transgenic plant seed according to claim 19, wherein  
the nucleic acid molecule encodes a protein or polypeptide comprising an amino  
acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4,  
SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID  
15           NO:14.

20           24.     The transgenic plant seed according to claim 19, wherein  
the nucleic acid molecule encodes a protein or polypeptide having a molecular  
mass of about 56 kDa to about 76 kDa.

25           25.     The transgenic plant seed according to claim 19, wherein  
the plant seed is selected from the group consisting of Gramineae, Liliaceae,  
Iridaceae, Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae,  
Rosaceae, Leguminosae, Malvaceae, Umbelliferae, Labiateae, Solanaceae,  
Cucurbitaceae, Compositae, and Rubiaceae.

30           26.     A method for enhancing tuber development in a plant  
comprising:  
                transforming a tuberous plant with a first DNA construct  
comprising:  
                a first nucleic acid molecule encoding a BEL transcription  
factor or a KNOX transcription factor, and

a first operably linked promoter and first 3' regulatory region,  
whereby tuber development in the plant is enhanced.

5           27. The method according to claim 26, wherein the first nucleic acid molecule encodes a BEL transcription factor.

10          28. The method according to claim 27, wherein the BEL transcription factor is from *Solanum tuberosum*.

15          29. The method according to claim 28, wherein the first nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

15          30. The method according to claim 28, wherein the first nucleic acid molecule encodes a protein that is at least 85% similar to a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis.

25          31. The method according to claim 28, wherein the first nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent conditions characterized by a hybridization buffer comprising 5X SSC at a temperature of 55°C.

30          32. The method according to claim 28, wherein the first nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

33. The method according to claim 28, wherein the first nucleic acid molecule encodes a protein or polypeptide having a molecular mass of about 56 kDa to about 76 kDa.

5 34. The method according to claim 26, wherein the first nucleic acid molecule encodes a KNOX transcription factor.

35. The method according to claim 34, wherein the KNOX transcription factor is from *Solanum tuberosum*.

10 36. The method according to claim 35, wherein the first nucleic acid molecule has a nucleotide sequence of SEQ ID NO:16.

15 37. The method according to claim 35, wherein the first nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:16 under stringent conditions characterized by a hybridization buffer comprising 5X SSC at a temperature of 55°C.

20 38. The method according to claim 35, wherein the first nucleic acid molecule encodes a protein or polypeptide having an amino acid sequence of SEQ ID NO:17.

25 39. The method according to claim 26, wherein the first DNA construct comprises a first nucleic acid molecule encoding a BEL transcription factor and a second nucleic acid molecule encoding a KNOX transcription factor.

30 40. The method according to claim 39, wherein the BEL transcription factor and the KNOX transcription factor are from *Solanum tuberosum*.

41. The method according to claim 26, wherein the first nucleic acid molecule encodes a BEL transcription factor and the method further comprises:

transforming the tuberous plant with a second DNA construct comprising:

a second nucleic acid molecule encoding a KNOX transcription factor, and  
5                   a second operably linked promoter and second 3' regulatory region.

42.       The method according to claim 26, wherein the tuberous plant is selected from the group consisting of potato, wild potato, dahlia, 10 caladium, Jerusalem artichoke, yam, sweet potato, cassava, tuberous begonia, and cyclamen.

43.       A method for enhancing growth in a plant comprising:  
transforming a plant with a DNA construct comprising:  
15                   a nucleic acid molecule encoding a BEL transcription factor from *Solanum tuberosum*, and  
                         an operably linked promoter and 3' regulatory region,  
whereby growth in the plant is enhanced.

20                  44.       The method according to claim 43, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

25                  45.       The method according to claim 43, wherein the nucleic acid molecule encodes a protein that is at least 85% similar to a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis.

30                  46.       The method according to claim 43, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13

under stringent conditions characterized by a hybridization buffer comprising 5X SSC at a temperature of 55°C.

47. The method according to claim 43, wherein the nucleic acid  
5 molecule encodes a protein or polypeptide comprising an amino acid sequence  
selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID  
NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

48. The method according to claim 43, wherein the first nucleic  
10 acid molecule encodes a protein or polypeptide having a molecular mass of about  
56 kDa to about 76 kDa.

49. The method according to claim 43, wherein the plant is  
selected from the group consisting of Gramineae, Liliaceae, Iridaceae,  
15 Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae, Rosaceae,  
Leguminosae, Malvaceae, Umbelliferae, Labiatae, Solanaceae, Cucurbitaceae,  
Compositae, and Rubiaceae.

50. A method for regulating flowering in a plant comprising:  
20 transforming a plant with a DNA construct comprising:  
a nucleic acid molecule encoding a BEL transcription factor  
from *Solanum tuberosum*, and  
an operably linked promoter and 3' regulatory region,  
whereby flowering in the plant is regulated.

25  
51. The method according to claim 50, wherein the nucleic acid  
molecule has a nucleotide sequence selected from the group consisting of SEQ ID  
NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID  
NO:11, and SEQ ID NO:13.

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52. The method according to claim 50, wherein the nucleic acid  
molecule encodes a protein that is at least 85% similar to a homeodomain region,  
a SKY box, a BELL domain, and a VSLTLGL-box in either SEQ ID NO:2, SEQ

ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis.

53. The method according to claim 50, wherein the nucleic acid  
5 molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3,  
SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13  
under stringent conditions characterized by a hybridization buffer comprising 5X  
SSC at a temperature of 55°C.

10 54. The method according to claim 50, wherein the nucleic acid  
molecule encodes a protein or polypeptide comprising an amino acid sequence  
selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID  
NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

15 55. The method according to claim 50, wherein the first nucleic  
acid molecule encodes a protein or polypeptide having a molecular mass of about  
56 kDa to about 76 kDa.

20 56. The method according to claim 50, wherein the plant is  
selected from the group consisting of Gramineae, Liliaceae, Iridaceae,  
Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae, Rosaceae,  
Leguminosae, Malvaceae, Umbelliferae, Labiate, Solanaceae, Cucurbitaceae,  
Compositae, and Rubiaceae.